

Yokota Sequence
SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION NARA INSTITUTE OF SCIENCE
AND TECHNOLOGY
RESEARCH INSTITUTE OF INNOVATIVE TECHNOLOGY FOR THE EARTH
KINKI UNIVERSITY
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SHIGEOKA, Shigeru
TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST
TECHNOLOGY

<130> 2006_1303A

<140> US 10/591,752

<141> 2006-09-01

<150> PCT/JP2005/004037

<151> 2005-03-02

<150> JP 2004-059513

<151> 2004-03-03

<160> 18

<170> PatentIn version 3.4

<210> 1

<211> 358

<212> PRT

<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

<400> 1

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met
20 25 30

Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser
35 40 45

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser
50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln
65 70 75 80

Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg
85 90 95

Yokota Sequence

Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro
100 105 110

Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp
115 120 125

Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser
130 135 140

Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp
145 150 155 160

His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val
165 170 175

Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met
180 185 190

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr
195 200 205

Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu
210 215 220

Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly
225 230 235 240

Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu
245 250 255

Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly
260 265 270

Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr
275 280 285

Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu
290 295 300

Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys
305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile
325 330 335

His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys
340 345 350

Yokota Sequence

Leu Glu Lys Tyr Leu Ala
355

<210> 2
<211> 1074
<212> DNA
<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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gaaacactaa caggctggct gcttaaacia gaaatggcag gtgttattga tgctgaactt	120
accatcgttc tttctagcat ttcattggct tgtaaaciaa ttgcttcctt ggttcaacga	180
gctgggtattt ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag	240
aagaaacttg atgttgtctc caatgaggtg ttttcgagct gcttgagatc gagtggaaga	300
acaggaataa tagcatcaga agaagaggat gtaccagtgg cagtggaaga gagttactct	360
ggaaactata ttgttgtgtt tgatccactt gatggttcat ccaacattga tgcagctgtc	420
tccactgggtt ccatcttttg catttatagc cctaacgatg agtgcattgt tgactctgat	480
cacgacgatg agtcacagct aagtgcagaa gaacagaggt gtgtagtgaa tgtatgtcaa	540
ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgta	600
cttacaattg gtaaagggtgt gtatgcattc acattagatc caatgtatgg tgaattcgta	660
ctcacttcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt	720
aactacaaaa tgtgggatga taaattgaag aagtacatgg atgatcttaa agagccagga	780
gagtcacaga aaccgtactc gtctcgttac ataggaggtt tagttgggga ctttcataga	840
acacttttat atggtgggat ttatggttac ccaagagatg caaagagtaa gaatgggaaa	900
ttgaggcttt tgtatgaatg tgcacctatg agttttattg ttgaacaagc tgggtggtaaa	960
ggttctgatg gtcacaaag aattcttgac attcaacca ccgagataca tcaacgtgtg	1020
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<210> 3
<211> 333
<212> PRT
<213> Spinacia oleracea L

<220>

<223> sedoheptulose-1, 7-bisphosphatase

Yokota Sequence

<400> 3

Val Asn Lys Ala Lys Asn Ser Ser Leu Val Thr Lys Cys Glu Leu Gly
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Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu
20 25 30

Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe
35 40 45

Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe
50 55 60

Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe
65 70 75 80

Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu
85 90 95

Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser
100 105 110

Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe
115 120 125

Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly
130 135 140

Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro
145 150 155 160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln
225 230 235 240

Yokota Sequence

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr
290 295 300

Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser
305 310 315 320

Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala
325 330

<210> 4
<211> 999
<212> DNA
<213> Spinacia oleracea L

<220>

<223> sedoheptulose-1,7-bisphosphatase

<400> 4

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggttg aactcaatgt	180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc	240
gaggcattga actattcaca cttctgcaag tatgcttggt cagaagaact ccctgagctt	300
caagatatgg gaggccccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga	360
tccagcattg tcgataccaa tttctcagtt gggaccatat tcgggggttg gccaggtgac	420
aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggtcct	480
aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt	540
gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc	600
tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac	660
tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgtaaccag	720
atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag	780
ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tggtggtcac	840

Yokota Sequence

agcagtgagg gaaccaagtc tgtgttggac attgaagtca aaaaccttga tgacagaacc 900
 caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc 960
 tctaggctag aggagccagt tcctgttgga gctgctgct 999

<210> 5
 <211> 356
 <212> PRT
 <213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from
 Synechococcus PCC 7942

<400> 5

Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala
 1 5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
 20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
 35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
 50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
 65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
 85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
 100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
 115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
 130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
 145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
 165 170 175

Yokota Sequence

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile
260 265 270

Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln
275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu
290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile
305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe
325 330 335

Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp
340 345 350

Arg Pro Glu Arg
355

<210> 6
<211> 1312
<212> DNA
<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from
Synechococcus PCC 7942

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Yokota Sequence

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cgaaaagaat gaagccgatc gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt	240
ggaaatgctg ggccgcatcg tcatcgggtga aggcgagcgc gacgaagcac cgatgctcta	300
tatcggtgaa gaagtgggca tctaccgcga tgcagacaag cgggctggcg taccggctgg	360
caagctgggtg gaaatcgaca tcgccgttga cccctgcgaa ggcaccaacc tctgcgccta	420
cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc	480
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aataaagtcc gcgaccgaaa acctgaaaat tctctcgga tgtctcgatc gcgccatcga	600
tgaattggtg gtcgtggtca tggatcgtcc ccgccacaaa gagctaattc aagagatccg	660
ccaagcgggt gccgcgtcc gtctgatcag cgatggtgac gtttcggccg cgatctcctg	720
cggttttgct ggcaccaaca cccacgccct gatgggcatc ggtgcagctc ccgagggtgt	780
gatttcggca gcagcaatgc gttgcctcgg cgggcacttc caaggccagc tgatctacga	840
cccagaagtg gtcaaaaccg gcctgatcgg tgaaagccgt gagagcaaca tcgctcgcct	900
gcaagaaatg ggcatacccg atccccgatc tgtctacgac gcgaacgaac tggcttcggg	960
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tgtttttcag cgaatccatt tgcgatcgt tttcaaacc ttttttcgtc aaccttcttt	1260
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 <211> 133
 <212> DNA
 <213> Nicotiana tabacum

<220>

<223> psbA promoter

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aagccttcca ttttctatct tgatttgtag aaaactagtg tgcttgggag tccctgatga	120
ttaaataaac caa	133

<210> 8
 <211> 159

Yokota Sequence

<212> DNA
<213> *Nicotiana tabacum*

<220>

<223> rps16 terminator

<400> 8
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tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct 120
atttgtattt ttttatcatt gcttccattg aattactag 159

<210> 9
<211> 805
<212> DNA
<213> *Escherichia coli*

<220>

<223> aadA

<400> 9
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gcgatcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtag ggctccgcag 120
tggtatggcgg cctgaagcca cacagtgata ttgatttgct gggtacgggtg accgtaaggc 180
ttgatgaaac aacgcggcga gctttgatca acgacctttt ggaaacttcg gcttcccctg 240
gagagagcga gattctccgc gctgtagaag tcaccattgt tgtgcacgac gacatcattc 300
cgtggcggtta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacattc 360
ttgcaggtat cttcgagcca gccacgatcg acattgatct ggctatcttg ctgacaaaag 420
caagagaaca tagcgttgcc ttggtagggtc cagcggcgga ggaactcttt gatccgggtt 480
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taaccggcaa aatcgcgccg aaggatgtcg ctgccgactg ggcaatggag cgcctgccgg 660
cccagtatca gcccgtcata cttgaagcta gacaggctta tcttggacaa gaagaagatc 720
gcttggcctc gcgcgcagat cagttggaag aatttgtcca ctacgtgaaa ggcgagatca 780
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<210> 10
<211> 4591
<212> DNA
<213> Artificial sequence

<220>

<223> synthetic construct

Yokota Sequence

<220>

<223> pLD6

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ggtttcgcca	cctctgactt	gagcgtcgat	ttttgtgatg	ctcgtcaggg	gggcggagcc	1740

Yokota Sequence

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Yokota Sequence

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ggccc	gcacc	gatcg	ccctt	cccaac	agtt	gcgcag	cctg	aatgg	cgaat	gggac	gcgcc	4140
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tgcc	agcgcc	ctagc	gccc	ctcctt	tcgc	tttctt	ccct	tccttt	ctcg	ccacg	ttcgc	4260
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gttcc	aaact	ggaaca	acac	tcaacc	ctat	ctcgg	tctat	tctttt	tgatt	tataa	gggat	4500
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<210> 11
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic construct

<220>
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		51

<210> 12
 <211> 142
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <223> rrn promoter

<400>	12	
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Yokota Sequence

gacgtgaggg ggcagggatg gctatatattc tgggagcgaa ctccgggcca atttgaagcg	120
cttgataca gttgtaggga gg	142

<210> 13
 <211> 390
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <223> psbA terminator

<400> 13 gatcctggcc tagtctatag gaggttttga aaagaaagga gcaataatca ttttcttggt	60
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acttacatag acttttttgt ttacattata gaaaaagaag gagagggtat tttcttgcat	180
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<210> 14
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 <213> Artificial sequence

<220>
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<220>
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<400> 14 tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacgggtca	60
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acaaattgac ttattatact cctgagtacc aaaccaagga tactgatata ttggcagcat	540
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Yokota Sequence

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ttgtaggtaa	cgtatttggg	ttcaaagccc	tgcgcgctct	acgtctggaa	gatctgcgaa	840
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Yokota Sequence

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cagattacgc	gcagaaaaaa	aggatctcaa	gaagatcctt	tgatcttttc	tacgggggtct	4380

Yokota Sequence

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<210> 15
 <211> 1434
 <212> DNA
 <213> *Nicotiana tabacum*

<220>
 <223> rbcL

<400> 15	
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cgagtaactc ctcaacctgg agttccacct gaagaagcag gggccgcggt agctgccgaa	180
tcttctactg gtacatggac aactgtatgg accgatggac ttaccagcct tgatcgttac	240
aaagggcgat gctaccgcat cgagcgtggt gttggagaaa aagatcaata tattgcttat	300

Yokota Sequence

gtagcttacc ctttagacct ttttgaagaa ggttctgtta ccaacatggt tacttccatt	360
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<210> 16
 <211> 705
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <223> accD

<400> 16	
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Yokota Sequence

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<210> 17
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic construct

<220>
<223> polylinker

<400> 17
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21

<210> 18
<211> 7
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic construct

<220>
<223> Shine-Dalgarno sequence

<400> 18
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